RAW SEQUENCE LISTING

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Application Serial Number: _10/541,947_

Source: _Pu7/10_

Date Processed by STIC: _7/21/05_

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RAW SEQUENCE LISTING   DATE: 07/21/2005
PATENT APPLICATION: US/10/541,947   TIME: 09:19:30

Input Set : D:\297-204 PCT.ST25.txt
Output Set: N:\CRF4\07212005\J541947.raw

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 3 <110> APPLICANT: North Carolina State University
 4        Petitte, James
 5        Pardue, Samuel
 7 <120> TITLE OF INVENTION: DEPLETION OF ENDOGENOUS PRIMORDIAL GERM CELLS IN AVIAN
SPECIES
 9 <130> FILE REFERENCE: 297/204 PCT
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/541,947
C--> 11 <141> CURRENT FILING DATE: 2005-07-08
   11 <150> PRIOR APPLICATION NUMBER: US 60/440,424
   12 <151> PRIOR FILING DATE: 2003-01-16
   14 <160> NUMBER OF SEQ ID NOS: 8
   16 <170> SOFTWARE: PatentIn version 3.2
   18 <210> SEQ ID NO: 1
   19 <211> LENGTH: 1989
   20 <212> TYPE: DNA
   21 <213> ORGANISM: Gallus gallus
   24 <220> FEATURE:
   25 <221> NAME/KEY: CDS
   26 <222> LOCATION: (1)..(1989)
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   31 1               5                  10                  15
   33 tcc cag ggg cgt tct gag gag cag gcg tgg atg gct aac tct ggc aga        96
   34 Ser Gln Gly Arg Ser Glu Glu Gln Ala Trp Met Ala Asn Ser Gly Arg
   35             20                  25                  30
   37 cca aac agc cca tcc ctc cgc ttc tcc agc aga cca agc agc ccc ttg       144
   38 Pro Asn Ser Pro Ser Leu Arg Phe Ser Ser Arg Pro Ser Ser Pro Leu
   39             35                  40                  45
   41 tct ggc ttc cca ggc aga cca aac agc ccc ttc ttt ggc ttt agt cag       192
   42 Ser Gly Phe Pro Gly Arg Pro Asn Ser Pro Phe Phe Gly Phe Ser Gln
   43     50                  55                  60
   45 aat aaa ggc tca ctt ggt gct aat gaa gga ctt aac aga agt·ctg cct       240
   46 Asn Lys Gly Ser Leu Gly Ala Asn Glu Gly Leu Asn Arg Ser Leu Pro
   47 65                  70                  75                  80
   49 gtg cag cat gac att gga gga tat tct ggg agc aga gag tct gtt gta       288
   50 Val Gln His Asp Ile Gly Gly Tyr Ser Gly Ser Arg Glu Ser Val Val
   51                 85                  90                  95
   53 cgt caa aac aga gaa gat caa cca gtg act aga ttt ggt aga ggg agg       336
   54 Arg Gln Asn Arg Glu Asp Gln Pro Val Thr Arg Phe Gly Arg Gly Arg
   55             100                 105                 110
   57 agt tct gga agc aga gat ttt caa gag agg aac tct gca aat gat cct       384
   58 Ser Ser Gly Ser Arg Asp Phe Gln Glu Arg Asn Ser Ala Asn Asp Pro
   59             115                 120                 125
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62 Gly Met Gln Asp Gln Gly Phe Arg Arg Val Pro Gly Ile Phe Gly Gln
63     130               135               140
65 agc aag tgt ttt aac agt gag gaa aga aat agt cct ctg cgt ggc agc    480
66 Ser Lys Cys Phe Asn Ser Glu Glu Arg Asn Ser Pro Leu Arg Gly Ser
67 145               150               155               160
69 cct ttt gcc cca gga gga aga gga gca gtt gga ggt cct gca gga gtt    528
70 Pro Phe Ala Pro Gly Gly Arg Gly Ala Val Gly Gly Pro Ala Gly Val
71               165               170               175
73 ctc aaa gga cgc tct gaa gaa att gat tct gga aga ggt cca aag gtg    576
74 Leu Lys Gly Arg Ser Glu Glu Ile Asp Ser Gly Arg Gly Pro Lys Val
75               180               185               190
77 act tat gtc ccc cct cct cca cct gaa gat gaa cag tcc atc ttt gca    624
78 Thr Tyr Val Pro Pro Pro Pro Pro Glu Asp Glu Gln Ser Ile Phe Ala
79               195               200               205
81 tgt tat cag tca gga att aat ttt gac aag tat gat gaa tgt gct gtt    672
82 Cys Tyr Gln Ser Gly Ile Asn Phe Asp Lys Tyr Asp Glu Cys Ala Val
83     210               215               220
85 gag atg tca gga ctt gac cct cca gca cca tta ctg gct ttt gaa gaa    720
86 Glu Met Ser Gly Leu Asp Pro Pro Ala Pro Leu Leu Ala Phe Glu Glu
87 225               230               235               240
89 gct aac ttt gct cag act tta agg aag aat ata tct aaa act gga tat    768
90 Ala Asn Phe Ala Gln Thr Leu Arg Lys Asn Ile Ser Lys Thr Gly Tyr
91               245               250               255
93 tca aaa ctt act cca gtg cag aag cac agc att cct gtt ata caa gca    816
94 Ser Lys Leu Thr Pro Val Gln Lys His Ser Ile Pro Val Ile Gln Ala
95               260               265               270
97 ggg cgg gat tta atg tca tgt gcc cag aca gga tca gga aaa aca gca    864
98 Gly Arg Asp Leu Met Ser Cys Ala Gln Thr Gly Ser Gly Lys Thr Ala
99               275               280               285
101 gct ttt ctt cta cca att gtg gac cgg atg atg aaa gat ggt gta act    912
102 Ala Phe Leu Leu Pro Ile Val Asp Arg Met Met Lys Asp Gly Val Thr
103     290               295               300
105 gca agc ttc cca aag cag caa gac cca caa tgc att att gtt gca cca    960
106 Ala Ser Phe Pro Lys Gln Gln Asp Pro Gln Cys Ile Ile Val Ala Pro
107 305               310               315               320
109 act aga gaa ctg ata aat cag atc ttc tta gaa gca agg aag ttt gtg    1008
110 Thr Arg Glu Leu Ile Asn Gln Ile Phe Leu Glu Ala Arg Lys Phe Val
111               325               330               335
113 tat ggg act tgt ata agg cct gtt gtg atc tat gga ggt aca cag aca    1056
114 Tyr Gly Thr Cys Ile Arg Pro Val Val Ile Tyr Gly Gly Thr Gln Thr
115     340               345               350
117 ggt cat tca atc cgt caa ata atg caa ggc tgt aat ata tta tgt gcc    1104
118 Gly His Ser Ile Arg Gln Ile Met Gln Gly Cys Asn Ile Leu Cys Ala
119               355               360               365
121 act cct gga agg ctt ctt gac att att gaa aaa ggg aag atc agt ttg    1152
122 Thr Pro Gly Arg Leu Leu Asp Ile Ile Glu Lys Gly Lys Ile Ser Leu
123     370               375               380
125 gtg gag gtg aaa tat ttg gta cta gat gaa gca gac cgc atg ctc gat    1200
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129 atg ggt ttt gga tta gat atg aag aag ctg att tct tat cca gaa atg      1248
130 Met Gly Phe Gly Leu Asp Met Lys Lys Leu Ile Ser Tyr Pro Glu Met
131               405               410               415
133 cca tct aaa gac aga cgt caa aca tta atg ttt agt gcc act ttt cct      1296
134 Pro Ser Lys Asp Arg Arg Gln Thr Leu Met Phe Ser Ala Thr Phe Pro
135               420               425               430
137 gag gaa gtt caa agg ctg gct ggt gaa ttt ttg aaa acg gac tat ata      1344
138 Glu Glu Val Gln Arg Leu Ala Gly Glu Phe Leu Lys Thr Asp Tyr Ile
139           435               440               445
141 ttt ctt gtt att gga aat acc tgt gga gcc tgc agt gat gtt cag caa      1392
142 Phe Leu Val Ile Gly Asn Thr Cys Gly Ala Cys Ser Asp Val Gln Gln
143           450               455               460
145 aat att ctt cag gtt ccc cgg tta tcc aag agg gat aaa cta ata gaa      1440
146 Asn Ile Leu Gln Val Pro Arg Leu Ser Lys Arg Asp Lys Leu Ile Glu
147 465               470               475               480
149 att cta caa agc aca ggt ggt gaa cga acc atg gtg ttt gtg gac aca      1488
150 Ile Leu Gln Ser Thr Gly Gly Glu Arg Thr Met Val Phe Val Asp Thr
151               485               490               495
153 aag aaa aaa gca gat tac ctt gca gcc ttt ctt tgt caa gag aac cta      1536
154 Lys Lys Lys Ala Asp Tyr Leu Ala Ala Phe Leu Cys Gln Glu Asn Leu
155           500               505               510
157 cca tcc acc agc att cat gga gat agg gaa cag aga gag aga gag ata      1584
158 Pro Ser Thr Ser Ile His Gly Asp Arg Glu Gln Arg Glu Arg Glu Ile
159           515               520               525
161 gct ctt cgc gat ttc cgt tct gga aaa tgt caa att ctt gtg gca act      1632
162 Ala Leu Arg Asp Phe Arg Ser Gly Lys Cys Gln Ile Leu Val Ala Thr
163           530               535               540
165 tcg gta gca tca aga ggc ctg gat att gaa aat gtt caa cat gtt att      1680
166 Ser Val Ala Ser Arg Gly Leu Asp Ile Glu Asn Val Gln His Val Ile
167 545               550               555               560
169 aat ttt gat ctc cct aac acc att gaa gat tat gta cat cga att gga      1728
170 Asn Phe Asp Leu Pro Asn Thr Ile Glu Asp Tyr Val His Arg Ile Gly
171               565               570               575
173 cga act ggt cgt tgt gga aat act ggc aaa gca gtt tca ttc ttt gat      1776
174 Arg Thr Gly Arg Cys Gly Asn Thr Gly Lys Ala Val Ser Phe Phe Asp
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177 gat cag tca gat ggc cat ctt gta caa tca cta ctt aaa gtg ctt tcc      1824
178 Asp Gln Ser Asp Gly His Leu Val Gln Ser Leu Leu Lys Val Leu Ser
179           595               600               605
181 aga acc cag cag gaa ttc cag ttt ggt gga aga atg gct gtc caa aga      1872
182 Arg Thr Gln Gln Glu Phe Gln Phe Gly Gly Arg Met Ala Val Gln Arg
183       610               615               620
185 aca aat att gtt gct tca act tgg tgc cca aag gga tta atg cag gcc      1920
186 Thr Asn Ile Val Ala Ser Thr Trp Cys Pro Lys Gly Leu Met Gln Ala
187 625               630               635               640
189 gtg gca gaa tgg aac cca aga gaa atg agg atg tca tat tct gaa aca      1968
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213 Pro Asn Ser Pro Ser Leu Arg Phe Ser Ser Arg Pro Ser Ser Pro Leu
214         35                40                45
217 Ser Gly Phe Pro Gly Arg Pro Asn Ser Pro Phe Phe Gly Phe Ser Gln
218     50                55                60
221 Asn Lys Gly Ser Leu Gly Ala Asn Glu Gly Leu Asn Arg Ser Leu Pro
222 65                70                75                80
225 Val Gln His Asp Ile Gly Gly Tyr Ser Gly Ser Arg Glu Ser Val Val
226             85                90                95
229 Arg Gln Asn Arg Glu Asp Gln Pro Val Thr Arg Phe Gly Arg Gly Arg
230             100               105               110
233 Ser Ser Gly Ser Arg Asp Phe Gln Glu Arg Asn Ser Ala Asn Asp Pro
234         115               120               125
237 Gly Met Gln Asp Gln Gly Phe Arg Arg Val Pro Gly Ile Phe Gly Gln
238     130               135               140
241 Ser Lys Cys Phe Asn Ser Glu Glu Arg Asn Ser Pro Leu Arg Gly Ser
242 145               150               155               160
245 Pro Phe Ala Pro Gly Gly Arg Gly Ala Val Gly Gly Pro Ala Gly Val
246             165               170               175
249 Leu Lys Gly Arg Ser Glu Glu Ile Asp Ser Gly Arg Gly Pro Lys Val
250         180               185               190
253 Thr Tyr Val Pro Pro Pro Pro Glu Asp Glu Gln Ser Ile Phe Ala
254     195               200               205
257 Cys Tyr Gln Ser Gly Ile Asn Phe Asp Lys Tyr Asp Glu Cys Ala Val
258     210               215               220
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262 225               230               235               240
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266         245               250               255
269 Ser Lys Leu Thr Pro Val Gln Lys His Ser Ile Pro Val Ile Gln Ala
270         260               265               270
273 Gly Arg Asp Leu Met Ser Cys Ala Gln Thr Gly Ser Gly Lys Thr Ala
274         275               280               285
277 Ala Phe Leu Leu Pro Ile Val Asp Arg Met Met Lys Asp Gly Val Thr
278     290               295               300
281 Ala Ser Phe Pro Lys Gln Gln Asp Pro Gln Cys Ile Ile Val Ala Pro
282 305               310               315               320
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286             325             330             335
289 Tyr Gly Thr Cys Ile Arg Pro Val Val Ile Tyr Gly Gly Thr Gln Thr
290             340             345             350
293 Gly His Ser Ile Arg Gln Ile Met Gln Gly Cys Asn Ile Leu Cys Ala
294             355             360             365
297 Thr Pro Gly Arg Leu Leu Asp Ile Ile Glu Lys Gly Lys Ile Ser Leu
298     370             375             380
301 Val Glu Val Lys Tyr Leu Val Leu Asp Glu Ala Asp Arg Met Leu Asp
302 385             390             395             400
305 Met Gly Phe Gly Leu Asp Met Lys Lys Leu Ile Ser Tyr Pro Glu Met
306             405             410             415
309 Pro Ser Lys Asp Arg Arg Gln Thr Leu Met Phe Ser Ala Thr Phe Pro
310             420             425             430
313 Glu Glu Val Gln Arg Leu Ala Gly Glu Phe Leu Lys Thr Asp Tyr Ile
314             435             440             445
317 Phe Leu Val Ile Gly Asn Thr Cys Gly Ala Cys Ser Asp Val Gln Gln
318     450             455             460
321 Asn Ile Leu Gln Val Pro Arg Leu Ser Lys Arg Asp Lys Leu Ile Glu
322 465             470             475             480
325 Ile Leu Gln Ser Thr Gly Gly Glu Arg Thr Met Val Phe Val Asp Thr
326             485             490             495
329 Lys Lys Lys Ala Asp Tyr Leu Ala Ala Phe Leu Cys Gln Glu Asn Leu
330             500             505             510
333 Pro Ser Thr Ser Ile His Gly Asp Arg Glu Gln Arg Glu Arg Glu Ile
334             515             520             525
337 Ala Leu Arg Asp Phe Arg Ser Gly Lys Cys Gln Ile Leu Val Ala Thr
338     530             535             540
341 Ser Val Ala Ser Arg Gly Leu Asp Ile Glu Asn Val Gln His Val Ile
342 545             550             555             560
345 Asn Phe Asp Leu Pro Asn Thr Ile Glu Asp Tyr Val His Arg Ile Gly
346             565             570             575
349 Arg Thr Gly Arg Cys Gly Asn Thr Gly Lys Ala Val Ser Phe Phe Asp
350             580             585             590
353 Asp Gln Ser Asp Gly His Leu Val Gln Ser Leu Leu Lys Val Leu Ser
354             595             600             605
357 Arg Thr Gln Gln Glu Phe Gln Phe Gly Gly Arg Met Ala Val Gln Arg
358     610             615             620
361 Thr Asn Ile Val Ala Ser Thr Trp Cys Pro Lys Gly Leu Met Gln Ala
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376 <213> ORGANISM: Gallus gallus
378 <400> SEQUENCE: 3
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VERIFICATION SUMMARY
PATENT APPLICATION: **US/10/541,947**

DATE: 07/21/2005
TIME: 09:19:31

Input Set : **D:\297-204 PCT.ST25.txt**
Output Set: **N:\CRF4\07212005\J541947.raw**

L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date